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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/669,781	09/24/2003	Juha Apajalahti	79428	6390

22242 7590 10/25/2006

FITCH EVEN TABIN AND FLANNERY  
120 SOUTH LA SALLE STREET  
SUITE 1600  
CHICAGO, IL 60603-3406

EXAMINER
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FRONDA, CHRISTIAN L

ART UNIT	PAPER NUMBER
----------	--------------

1652

DATE MAILED: 10/25/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

## Office Action Summary

Application No.

10/669,781

Applicant(s)

APAJALAHTI ET AL.

Examiner

Christian L. Fronda

Art Unit

1652

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 28 August 2006.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-12 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-12 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 24 October 2003 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☒ Certified copies of the priority documents have been received in Application No. 10/251,503.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- ☐ Notice of References Cited (PTO-892)
- ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- ☒ Information Disclosure Statement(s) (PTO/SB/08)  
Paper No(s)/Mail Date 08/23/06.
- ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_
- ☐ Notice of Informal Patent Application
- ☒ Other: RSL Error Report.

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### DETAILED ACTION

1. Claims 1-12 are pending and under consideration in this Office Action.
2. The rejection of claim 10 under 35 U.S.C. 112, second paragraph, as being indefinite has been withdrawn in view of applicants' arguments and amendment to the claim filed 08/28/2006.

### *NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES*

3. This application fails to comply with the requirements of 37 CFR §§ 1.821 through 1.825 for the reason(s) set forth: certain errors were detected by the STIC Biotechnology Systems Branch. Please see the attached paper RAW SEQUEUNCE LISTING ERROR REPORT.

### *Claim Rejections - 35 U.S.C. § 112, 1st Paragraph*

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:  
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.
5. Claims 1-12 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid of SEQ ID NO: 1, an isolated host cell transformed with a nucleic acid of SEQ ID NO: 1, and a method for identifying a nucleic acid molecule which encodes a phytase using SEQ ID NO: 1, and a method for the production of the nucleic acid sequence of SEQ ID NO: 1 using the specific PCR primers listed on page 25 of the specification; does not reasonably provide enablement for any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions and any method for the production of any nucleic acid which encodes a phytase using any two or more PCR primers which hybridize to SEQ ID NO: 1 or to any complement of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.  
Applicants' arguments filed 08/28/2006 have been fully considered but are not

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persuasive. The examiner respectfully disagrees with applicants' position that one of ordinary skill in the art would understand what conditions are needed to provide high stringency for Southern blotting.

The nature and breadth of the claims encompass any nucleic acid that hybridizes to SEQ ID NO: 1 under any high stringency conditions. Applicants have not sufficiently defined the conditions under which the hybridizations are to take place. Nucleic acid hybridization assays are extremely sensitive to the conditions in which they are performed. The buffer composition, pH, temperature, length of time, salt concentrations, quality and source of template nucleic acid, are all variables which determine the reproducibility of a given hybridization experiment.

Given the unpredictability of the art and the nature of hybridization experiments in general, it is not sufficient to merely cite hybridization without a clear and explicit recitation of the conditions associated with the hybridization. For example, the definition of stringency as it pertains to hybridization conditions is subject to interpretation and is different from laboratory to laboratory. Therefore, without a clear and explicit recitation of the conditions which were actually used by Applicants in isolating the claimed polynucleotides which hybridize to the disclosed sequences, the skilled artisan would not be able to practice the claimed invention and would not be reasonably apprised of the metes and bounds of the claimed invention. Without such guidance, the experimentation left to those skilled in the art is undue. Including in the claims the exact nature of the hybridization conditions, such as salt concentration and temperature, would aid in overcoming this portion of the rejection.

### *Conclusion*

6. No claim is allowed.

7. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire **THREE MONTHS** from the mailing date of this action. In the event a first reply is filed within **TWO MONTHS** of the mailing date of this final action and the advisory action is not mailed until after the end of the **THREE-MONTH** shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than **SIX MONTHS** from the mailing date of this final action.

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8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Christian L Fronda whose telephone number is (571)272-0929. The examiner can normally be reached Monday-Friday between 9:00AM - 5:00PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura N Achutamurthy can be reached on (571)272-0928. The fax phone number for the organization where this application or proceeding is assigned is (571)273-8300.

9. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

CLF

  
**TEKCHAND SAIDHA**  
**PRIMARY EXAMINER**

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/669,781A  
Source: 1fw16  
Date Processed by STIC: 8/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:33

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

3 <110> APPLICANT: Finnfeeds International, Ltd.  
 5 <120> TITLE OF INVENTION: Phytase from Bacillus subtilis, gene encoding said phytase,  
 6 method for its production and use  
 8 <130> FILE REFERENCE: 79428  
 10 <140> CURRENT APPLICATION NUMBER: 10/669,781A  
 11 <141> CURRENT FILING DATE: 2003-09-24  
 13 <160> NUMBER OF SEQ ID NOS: 36  
 15 <170> SOFTWARE: PatentIn version 3.3

*see pp 1-10*

## ERRORED SEQUENCES

E--> 17 <210> SEQ ID NO: ~~seq id no: 1~~

18 &lt;211&gt; LENGTH: 1290

19 &lt;212&gt; TYPE: DNA

20 &lt;213&gt; ORGANISM: Bacillus subtilis; Strain: B13

23 &lt;220&gt; FEATURE:

24 &lt;221&gt; NAME/KEY: CDS

25 &lt;222&gt; LOCATION: (91)..(1239)

ⓧ 27 <400> SEQUENCE: 1

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30 aagtgcacgt tcataaaagg aggaagtaaa atg aat cat tca aaa aca ctt ttg 114

31 Met Asn His Ser Lys Thr Leu Leu

32 1 5

34 tta acc gcg gcg gcc gga ctg atg ctc aca tgc ggt gcg gtg tct tcc 162

35 Leu Thr Ala Ala Ala Gly Leu Met Leu Thr Cys Gly Ala Val Ser Ser

36 10 15 20

38 cag gca aag cat aag ctg tcc gat cct tat cat ttt acc gtg aat gca 210

39 Gln Ala Lys His Lys Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala

40 25 30 35 40

42 gcg gcg gaa acg gaa ccg gtt gat acg gcc ggt gac gcg gct gat gat 258

43 Ala Ala Glu Thr Glu Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp

44 45 50 55

46 cct gcg att tgg ctg gac ccc aag act cct cag aac agc aaa ttg att 306

47 Pro Ala Ile Trp Leu Asp Pro Lys Thr Pro Gln Asn Ser Lys Leu Ile

48 60 65 70

50 acg acc aat aaa aaa tca ggt tta gtc gtt tac agc ctt gat ggt aag 354

51 Thr Thr Asn Lys Lys Ser Gly Leu Val Val Tyr Ser Leu Asp Gly Lys

52 75 80 85

54 atg ctt cat tcc tat aat acc ggg aag ctg aac aat gtc gat atc cgt 402

55 Met Leu His Ser Tyr Asn Thr Gly Lys Leu Asn Asn Val Asp Ile Arg

56 90 95 100

58 tat gat ttt ccg ttg aac ggc aaa aaa gtc gat atc gcg gca gca tcc 450

*do not insert alphabetical headings. The CRF software will insert them for clarity.*

*Does Not Comply  
Corrected Diskette Needed*

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:33

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Output Set: N:\CRF4\08302006\J669781A.raw

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60 105          110          115          120
62 aat cgg tct gaa gga aaa aat acc att gag att tac gct att gat gga      498
63 Asn Arg Ser Glu Gly Lys Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly
64          125          130          135
66 aaa aac ggc aca tta caa agc atg aca gat cca gac cat ccg att gca      546
67 Lys Asn Gly Thr Leu Gln Ser Met Thr Asp Pro Asp His Pro Ile Ala
68          140          145          150
70 aca gca att aat gag gta tac ggt ttt acc tta tac cac agt caa aaa      594
71 Thr Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Tyr His Ser Gln Lys
72          155          160          165
74 aca gga aaa tat tac gcg atg gtg aca gga aaa gag ggt gaa ttt gaa      642
75 Thr Gly Lys Tyr Tyr Ala Met Val Thr Gly Lys Glu Gly Glu Phe Glu
76          170          175          180
78 caa tac gaa tta aag gcg gac aaa aat gga tac ata tcc ggc aaa aag      690
79 Gln Tyr Glu Leu Lys Ala Asp Lys Asn Gly Tyr Ile Ser Gly Lys Lys
80 185          190          195          200
82 gta cgg gcg ttt aaa atg aat tcc cag acg gaa ggg atg gca gca gac      738
83 Val Arg Ala Phe Lys Met Asn Ser Gln Thr Glu Gly Met Ala Ala Asp
84          205          210          215
86 gat gaa tac ggc agg ctt tat atc gca gaa gaa gat gag gcc att tgg      786
87 Asp Glu Tyr Gly Arg Leu Tyr Ile Ala Glu Glu Asp Glu Ala Ile Trp
88          220          225          230
90 aag ttc agc gcc gag ccg gac ggc agt aac gga acg gtt atc gac      834
91 Lys Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp
92          235          240          245
94 cgt gcc gac ggc agg cat tta act cgt gat att gaa gga ttg acg att      882
95 Arg Ala Asp Gly Arg His Leu Thr Arg Asp Ile Glu Gly Leu Thr Ile
96          250          255          260
98 tac tac gct gct gac ggc aaa ggc tat ctg atg gca tca agc cag gga      930
99 Tyr Tyr Ala Ala Asp Gly Lys Gly Tyr Leu Met Ala Ser Ser Gln Gly
100 265          270          275          280
102 aac agc agc tac gcc att tat gac aga caa gga aag aac aaa tat gtt      978
103 Asn Ser Ser Tyr Ala Ile Tyr Asp Arg Gln Gly Lys Asn Lys Tyr Val
104          285          290          295
106 gcg gat ttt cgc ata aca gac ggt cct gaa aca gac ggg aca agc gat      1026
107 Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr Ser Asp
108          300          305          310
110 aca gac gga att gac gtt ctg ggt ttc gga ctg ggg cct gaa tat ccg      1074
111 Thr Asp Gly Ile Asp Val Leu Gly Phe Gly Leu Gly Pro Glu Tyr Pro
112          315          320          325
114 ttc ggt att ttt gtc gca cag gac ggt gaa aat ata gat cac ggc caa      1122
115 Phe Gly Ile Phe Val Ala Gln Asp Gly Glu Asn Ile Asp His Gly Gln
116          330          335          340
118 aag gcc aat caa aat ttt aaa atc gtg cca tgg gaa aga att gct gat      1170
119 Lys Ala Asn Gln Asn Phe Lys Ile Val Pro Trp Glu Arg Ile Ala Asp
120 345          350          355          360
122 caa atc ggt ttc cgc ctg gca aat gaa cag gtt gac ccg aga aaa      1218
123 Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp Pro Arg Lys

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Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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124          365          370          375
126 ctg acc gac aga agc gga aaa taaacatgca aaaagcagct tataacaagct      1269
127 Leu Thr Asp Arg Ser Gly Lys
128          380
130 gcttttttgca tgtgaagaac g      1290
E--> 133 <210> SEQ ID NO: SEQ ID NO: 2
134 <211> LENGTH: 383
135 <212> TYPE: PRT
136 <213> ORGANISM: Bacillus subtilis; Strain: B13
OK-> 138 <400> SEQUENCE: 2
140 Met Asn His Ser Lys Thr Leu Leu Leu Thr Ala Ala Ala Gly Leu Met
141 1          5          10          15
144 Leu Thr Cys Gly Ala Val Ser Ser Gln Ala Lys His Lys Leu Ser Asp
145          20          25          30
148 Pro Tyr His Phe Thr Val Asn Ala Ala Glu Thr Glu Pro Val Asp
149          35          40          45
152 Thr Ala Gly Asp Ala Ala Asp Pro Ala Ile Trp Leu Asp Pro Lys
153 50          55          60
156 Thr Pro Gln Asn Ser Lys Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu
157 65          70          75          80
160 Val Val Tyr Ser Leu Asp Gly Lys Met Leu His Ser Tyr Asn Thr Gly
161          85          90          95
164 Lys Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
165          100         105         110
168 Lys Val Asp Ile Ala Ala Ala Ser Asn Arg Ser Glu Gly Lys Asn Thr
169          115         120         125
172 Ile Glu Ile Tyr Ala Ile Asp Gly Lys Asn Gly Thr Leu Gln Ser Met
173          130         135         140
176 Thr Asp Pro Asp His Pro Ile Ala Thr Ala Ile Asn Glu Val Tyr Gly
177 145         150         155         160
180 Phe Thr Leu Tyr His Ser Gln Lys Thr Gly Lys Tyr Tyr Ala Met Val
181          165         170         175
184 Thr Gly Lys Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys Ala Asp Lys
185          180         185         190
188 Asn Gly Tyr Ile Ser Gly Lys Lys Val Arg Ala Phe Lys Met Asn Ser
189          195         200         205
192 Gln Thr Glu Gly Met Ala Ala Asp Asp Glu Tyr Gly Arg Leu Tyr Ile
193          210         215         220
196 Ala Glu Glu Asp Glu Ala Ile Trp Lys Phe Ser Ala Glu Pro Asp Gly
197 225         230         235         240
200 Gly Ser Asn Gly Thr Val Ile Asp Arg Ala Asp Gly Arg His Leu Thr
201          245         250         255
204 Arg Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Ala Ala Asp Gly Lys Gly
205          260         265         270
208 Tyr Leu Met Ala Ser Ser Gln Gly Asn Ser Ser Tyr Ala Ile Tyr Asp
209          275         280         285
212 Arg Gln Gly Lys Asn Lys Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly
213          290         295         300
216 Pro Glu Thr Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Leu Gly

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Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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217 305          310          315          320
220 Phe Gly Leu Gly Pro Glu Tyr Pro Phe Gly Ile Phe Val Ala Gln Asp
221          325          330          335
224 Gly Glu Asn Ile Asp His Gly Gln Lys Ala Asn Gln Asn Phe Lys Ile
225          340          345          350
228 Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala
229          355          360          365
232 Asn Glu Gln Val Asp Pro Arg Lys Leu Thr Asp Arg Ser Gly Lys
233          370          375          380
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237 <211> LENGTH: 25
238 <212> TYPE: PRT
239 <213> ORGANISM: Bacillus subtilis
E--> 241 <400> SEQUENCE: 3
243 Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
244 1          5          10          15
247 Pro Val Asp Thr Ala Gly Asp Ala Ala
248          20          25
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252 <211> LENGTH: 32
253 <212> TYPE: PRT
254 <213> ORGANISM: Bacillus subtilis
E--> 256 <400> SEQUENCE: 4
258 Leu Ser Asp Pro Tyr His Phe Thr Val Asn Ala Ala Ala Glu Thr Glu
259 1          5          10          15
262 Pro Val Asp Thr Ala Gly Asp Ala Ala Asp Asp Pro Ala Ile Leu Asp
263          20          25          30
E--> 266 <210> SEQ ID NO: SEQ ID NO:5
267 <211> LENGTH: 8
268 <212> TYPE: PRT
269 <213> ORGANISM: Bacillus subtilis
E--> 271 <400> SEQUENCE: 5
273 Tyr Tyr Ala Met Val Thr Gly Lys
274 1          5
E--> 277 <210> SEQ ID NO: SEQ ID NO:6
278 <211> LENGTH: 10
279 <212> TYPE: PRT
280 <213> ORGANISM: Bacillus subtilis
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284 Glu Gly Glu Phe Glu Gln Tyr Glu Leu Lys
285 1          5          10
E--> 288 <210> SEQ ID NO: SEQ ID NO:7
289 <211> LENGTH: 9
290 <212> TYPE: PRT
291 <213> ORGANISM: Bacillus subtilis
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295 Met Leu His Ser Tyr Asn Thr Gly Lys
296 1          5
E--> 299 <210> SEQ ID NO: SEQ ID NO:8

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## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

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300 <211> LENGTH: 6
301 <212> TYPE: PRT
302 <213> ORGANISM: Bacillus subtilis
EK-> 304 <400> SEQUENCE: 8
306 Ile Val Pro Trp Glu Arg
307 1 5
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311 <211> LENGTH: 25
312 <212> TYPE: PRT
313 <213> ORGANISM: Bacillus subtilis
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317 Ile Val Pro Trp Glu Arg Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu
318 1 5 10 15
321 Ala Asn Glu Gln Val Asp Pro Arg Lys
322 20 25
E--> 325 <210> SEQ ID NO: SEQ ID NO:10
326 <211> LENGTH: 30
327 <212> TYPE: PRT
328 <213> ORGANISM: Bacillus subtilis
EK-> 330 <400> SEQUENCE: 10
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333 1 5 10 15
336 Ala Ile Asn Glu Val Tyr Gly Phe Thr Leu Trp His Ser Gln
337 20 25 30
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341 <211> LENGTH: 23
342 <212> TYPE: PRT
343 <213> ORGANISM: Bacillus subtilis
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347 Tyr Val Ala Asp Phe Arg Ile Thr Asp Gly Pro Glu Thr Asp Gly Thr
348 1 5 10 15
351 Ser Asp Asp Asp Gly Ile Ile
352 20
E--> 355 <210> SEQ ID NO: SEQ ID NO:12
356 <211> LENGTH: 7
357 <212> TYPE: PRT
358 <213> ORGANISM: Bacillus subtilis
EK-> 360 <400> SEQUENCE: 12
362 Leu Thr Asp Arg Ser Gly Lys
363 1 5
E--> 366 <210> SEQ ID NO: SEQ ID NO:13
367 <211> LENGTH: 13
368 <212> TYPE: PRT
369 <213> ORGANISM: Bacillus subtilis
EK-> 371 <400> SEQUENCE: 13
373 Val Asp Ile Ala Ala Ser Asn Arg Ser Glu Gly Lys
374 1 5 10
E--> 377 <210> SEQ ID NO: SEQ ID NO:14
378 <211> LENGTH: 19

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## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

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Output Set: N:\CRF4\08302006\J669781A.raw

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380 <213> ORGANISM: Bacillus subtilis
EX-> 382 <400> SEQUENCE: 14
384 Ile Ala Asp Gln Ile Gly Phe Arg Pro Leu Ala Asn Glu Gln Val Asp
385 1 5 10 15
388 Pro Arg Lys
E--> 392 <210> SEQ ID NO: SEQ ID NO:15
393 <211> LENGTH: 6
394 <212> TYPE: PRT
EX-> 395 <213> ORGANISM: Bacillus subtilis
397 <400> SEQUENCE: 15
399 Ala Asn Gln Asn Phe Lys
400 1 5
E--> 403 <210> SEQ ID NO: SEQ ID NO:16
404 <211> LENGTH: 5
405 <212> TYPE: PRT
EX-> 406 <213> ORGANISM: Bacillus subtilis
408 <400> SEQUENCE: 16
410 Val Arg Ala Phe Lys
411 1 5
E--> 414 <210> SEQ ID NO: SEQ ID NO:17
415 <211> LENGTH: 11
416 <212> TYPE: PRT
EX-> 417 <213> ORGANISM: Bacillus subtilis
419 <400> SEQUENCE: 17
421 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro
422 1 5 10
E--> 425 <210> SEQ ID NO: SEQ ID NO:18
426 <211> LENGTH: 15
427 <212> TYPE: PRT
EX-> 428 <213> ORGANISM: Bacillus subtilis
430 <400> SEQUENCE: 18
432 Leu Asn Asn Val Asp Ile Arg Tyr Asp Phe Pro Leu Asn Gly Lys
433 1 5 10 15
E--> 436 <210> SEQ ID NO: SEQ ID NO:19
437 <211> LENGTH: 11
438 <212> TYPE: PRT
EX-> 439 <213> ORGANISM: Bacillus subtilis
441 <400> SEQUENCE: 19
443 Asn Thr Ile Glu Ile Tyr Ala Ile Asp Gly Lys
444 1 5 10
E--> 447 <210> SEQ ID NO: SEQ ID NO:20
448 <211> LENGTH: 11
449 <212> TYPE: PRT
EX-> 450 <213> ORGANISM: Bacillus subtilis
452 <400> SEQUENCE: 20
454 Ser Gly Leu Val Tyr Ser Leu Asp Gly Lys
455 1 5 10
E--> 458 <210> SEQ ID NO: SEQ ID NO:21

```

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

459 <211> LENGTH: 22
460 <212> TYPE: PRT
461 <213> ORGANISM: Bacillus subtilis
OK-> 463 <400> SEQUENCE: 21
465 Phe Ser Ala Glu Pro Asp Gly Gly Ser Asn Gly Thr Val Ile Asp Arg
466 1 5 10 15
469 Ala Asp Gly Arg His Leu
470 20
E--> 473 <210> SEQ ID NO: SEQ ID NO:22
474 <211> LENGTH: 23
475 <212> TYPE: DNA
476 <213> ORGANISM: Artificial
478 <220> FEATURE:
479 <223> OTHER INFORMATION: Synthesized
482 <220> FEATURE:
483 <221> NAME/KEY: modified_base
484 <222> LOCATION: (1)..(23)
485 <223> OTHER INFORMATION: All Ns represents inosine
OK-> 487 <400> SEQUENCE: 22
W--> 488 tcngatccnt atcattttac ngt 23
E--> 491 <210> SEQ ID NO: SEQ ID NO:23
492 <211> LENGTH: 23
493 <212> TYPE: DNA
494 <213> ORGANISM: Artificial
496 <220> FEATURE:
497 <223> OTHER INFORMATION: Synthesized
500 <220> FEATURE:
501 <221> NAME/KEY: modified_base
502 <222> LOCATION: (1)..(23)
503 <223> OTHER INFORMATION: N represents inosine
OK-> 506 <400> SEQUENCE: 23
507 agmaggaaaat catancyrat atc 23
E--> 510 <210> SEQ ID NO: SEQ ID NO:24
511 <211> LENGTH: 22
512 <212> TYPE: DNA
513 <213> ORGANISM: Artificial
515 <220> FEATURE:
516 <223> OTHER INFORMATION: Synthesized
518 <220> FEATURE:
519 <221> NAME/KEY: modified_base
520 <222> LOCATION: (1)..(22)
521 <223> OTHER INFORMATION: All N's represent inosine
OK-> 523 <400> SEQUENCE: 24
524 cttcnganck rttnngangcn gc 22
E--> 527 <210> SEQ ID NO: SEQ ID NO:25
528 <211> LENGTH: 20
529 <212> TYPE: DNA
530 <213> ORGANISM: Artificial
532 <220> FEATURE:

```

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

533 <223> OTHER INFORMATION: Synthesized
536 <220> FEATURE:
537 <221> NAME/KEY: modified_base
538 <222> LOCATION: (1)..(20)
539 <223> OTHER INFORMATION: All N's represent inosine
OK-> 541 <400> SEQUENCE: 25
542 tgatcngcra tnckttccca 20
E--> 545 <210> SEQ ID NO: SEQ ID NO+26
546 <211> LENGTH: 20
547 <212> TYPE: DNA
548 <213> ORGANISM: Artificial
550 <220> FEATURE:
551 <223> OTHER INFORMATION: Synthesized
OK-> 553 <400> SEQUENCE: 26
554 gcratmggat gatcmggatc 20
E--> 557 <210> SEQ ID NO: SEQ ID NO+27
558 <211> LENGTH: 21
559 <212> TYPE: DNA
560 <213> ORGANISM: Artificial
562 <220> FEATURE:
563 <223> OTHER INFORMATION: Synthesized
566 <220> FEATURE:
567 <221> NAME/KEY: modified_base
568 <222> LOCATION: (1)..(21)
569 <223> OTHER INFORMATION: N represents inosine
OK-> 571 <400> SEQUENCE: 27
572 ttcataytgt tcaaattcnc c 21
E--> 575 <210> SEQ ID NO: SEQ ID NO+28
576 <211> LENGTH: 26
577 <212> TYPE: DNA
578 <213> ORGANISM: Artificial
580 <220> FEATURE:
581 <223> OTHER INFORMATION: Synthesized
584 <220> FEATURE:
585 <221> NAME/KEY: modified_base
586 <222> LOCATION: (1)..(26)
587 <223> OTHER INFORMATION: All N's represent inosine
OK-> 589 <400> SEQUENCE: 28
590 ttncngtrt tatangaatg narcac 26
E--> 593 <210> SEQ ID NO: SEQ ID NO+29
594 <211> LENGTH: 20
595 <212> TYPE: DNA
596 <213> ORGANISM: Artificial
598 <220> FEATURE:
599 <223> OTHER INFORMATION: Synthesized
602 <220> FEATURE:
603 <221> NAME/KEY: modified_base
604 <222> LOCATION: (1)..(20)
605 <223> OTHER INFORMATION: N represents inosine

```

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

EX-> 607 <400> SEQUENCE: 29
      608 ccatcratng cataratttc
E--> 611 <210> SEQ ID NO: SEQ ID NO:30
      612 <211> LENGTH: 18
      613 <212> TYPE: DNA
      614 <213> ORGANISM: Artificial
      616 <220> FEATURE:
      617 <223> OTHER INFORMATION: Synthesized
      620 <220> FEATURE:
      621 <221> NAME/KEY: modified_base
      622 <222> LOCATION: (1)..(18)
      623 <223> OTHER INFORMATION: N represents inosine
EX-> 626 <400> SEQUENCE: 30
      627 tttaaartty tgrttngc
E--> 630 <210> SEQ ID NO: SEQ ID NO:31
      631 <211> LENGTH: 18
      632 <212> TYPE: DNA
      633 <213> ORGANISM: Artificial
      635 <220> FEATURE:
      636 <223> OTHER INFORMATION: Synthesized
      639 <220> FEATURE:
      640 <221> NAME/KEY: modified_base
      641 <222> LOCATION: (1)..(18)
      642 <223> OTHER INFORMATION: All N's represent inosine
EX-> 645 <400> SEQUENCE: 31
      646 tttncngtn accatngc
E--> 649 <210> SEQ ID NO: SEQ ID NO:32
      650 <211> LENGTH: 38
      651 <212> TYPE: DNA
      652 <213> ORGANISM: Artificial
      654 <220> FEATURE:
      655 <223> OTHER INFORMATION: Synthesized
      658 <220> FEATURE:
      659 <221> NAME/KEY: misc_feature
      660 <222> LOCATION: (21)..(21)
      661 <223> OTHER INFORMATION: n is a, c, g, or t
EX-> 663 <400> SEQUENCE: 32
      664 gayccdtayc ayttyacdgt naaygcdgcd gcdgaaac
E--> 667 <210> SEQ ID NO: SEQ ID NO:33
      668 <211> LENGTH: 52
      669 <212> TYPE: DNA
      670 <213> ORGANISM: Artificial
      672 <220> FEATURE:
      673 <223> OTHER INFORMATION: Synthesized
      676 <220> FEATURE:
      677 <221> NAME/KEY: misc_feature
      678 <222> LOCATION: (7)..(14)
      679 <223> OTHER INFORMATION: Mfe I site
      681 <220> FEATURE:

```

## RAW SEQUENCE LISTING

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:34

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

```

682 <221> NAME/KEY: RBS
683 <222> LOCATION: (14)..(19)
685 <220> FEATURE:
686 <221> NAME/KEY: CDS
687 <222> LOCATION: (27)..(50)
OK-> 689 <400> SEQUENCE: 33
690 gtttctcaat tgaaggagga atttaa atg ctg tcc gat cct tat cat ttt ac 52
691                               Met Leu Ser Asp Pro Tyr His Phe
692                               1           5
E--> 695 <210> SEQ ID NO: SEQ ID NO+34
696 <211> LENGTH: 8
697 <212> TYPE: PRT
698 <213> ORGANISM: Artificial
700 <220> FEATURE:
701 <223> OTHER INFORMATION: Synthetic Construct
OK-> 703 <400> SEQUENCE: 34
705 Met Leu Ser Asp Pro Tyr His Phe
706 1           5
E--> 709 <210> SEQ ID NO: SEQ ID NO+35
710 <211> LENGTH: 35
711 <212> TYPE: DNA
712 <213> ORGANISM: Artificial
714 <220> FEATURE:
715 <223> OTHER INFORMATION: Synthesized
718 <220> FEATURE:
719 <221> NAME/KEY: misc_feature
720 <222> LOCATION: (6)..(11)
721 <223> OTHER INFORMATION: Sal I site
OK-> 723 <400> SEQUENCE: 35
724 aataagtcga cgtagcaccg gattccggct gtgct 35
E--> 727 <210> SEQ ID NO: SEQ ID NO+36
728 <211> LENGTH: 34
729 <212> TYPE: DNA
730 <213> ORGANISM: Artificial
732 <220> FEATURE:
733 <223> OTHER INFORMATION: Synthesized
736 <220> FEATURE:
737 <221> NAME/KEY: misc_feature
738 <222> LOCATION: (6)..(11)
739 <223> OTHER INFORMATION: Bgl II site
OK-> 741 <400> SEQUENCE: 36
742 aataaagatc tttttccgct tctgtcggtc agtt 34

```



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/669,781A

DATE: 08/30/2006

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:27 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1  
L:133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:138 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2  
L:236 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:241 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:3  
L:251 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:256 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4  
L:266 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:271 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:5  
L:277 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:6  
L:288 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:293 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7  
L:299 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:304 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:8  
L:310 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:315 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:9  
L:325 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:330 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:10  
L:340 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:11  
L:355 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:360 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:12  
L:366 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:371 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:13  
L:377 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:14  
L:392 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:397 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:15  
L:403 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:16  
L:414 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:419 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:17  
L:425 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:430 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:18  
L:436 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:441 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:19  
L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:452 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:20  
L:458 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:463 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:21  
L:473 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:487 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:22  
L:488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
L:491 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:506 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:23  
M:341 Repeated in SeqNo=0

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VERIFICATION SUMMARY

DATE: 08/30/2006

PATENT APPLICATION: US/10/669,781A

TIME: 10:14:35

Input Set : F:\6031.79428 sequence.listing.ST25.txt

Output Set: N:\CRF4\08302006\J669781A.raw

L:510 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:523 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:24  
L:527 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:541 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:25